```
============================================================
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2008; month=7; day=11; hr=10; min=4; sec=1; ms=638; ]
============================================================
```

Validated By CRFValidator v 1.0.3

Application No: 10575114 Version No: 1.0

Input Set:

Output Set:

Started: 2008-06-09 13:56:57.099
Finished: 2008-06-09 13:56:59.402
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 303 ms
Total Warnings: 22
Total Errors: 4
No. of SeqIDs Defined: 43
Actual SeqID Count: 43

Error code		Error Description
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (18)
W	213	Artificial or Unknown found in <213> in SEQ ID (22)
W	213	Artificial or Unknown found in <213> in SEQ ID (23)
W	213	Artificial or Unknown found in <213> in SEQ ID (24)
W	213	Artificial or Unknown found in <213> in SEQ ID (25)
W	213	Artificial or Unknown found in <213> in SEQ ID (26)
W	213	Artificial or Unknown found in <213> in SEQ ID (27)
W	213	Artificial or Unknown found in <213> in SEQ ID (28)
W	213	Artificial or Unknown found in <213> in SEQ ID (29)
W	213	Artificial or Unknown found in <213> in SEQ ID (30)
W	213	Artificial or Unknown found in <213> in SEQ ID (31)
W	213	Artificial or Unknown found in <213> in SEQ ID (32)
W	213	Artificial or Unknown found in <213> in SEQ ID (33)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (33)
W	213	Artificial or Unknown found in <213> in SEQ ID (34)
W	213	Artificial or Unknown found in <213> in SEQ ID (35)
W	213	Artificial or Unknown found in <213> in SEQ ID (36)
W	213	Artificial or Unknown found in <213> in SEQ ID (37)

Input Set:

Output Set:

Started: 2008-06-09 13:56:57.099
Finished: 2008-06-09 13:56:59.402
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 303 ms
Total Warnings: 22
Total Errors: 4
No. of SeqIDs Defined: 43
Actual SeqID Count: 43

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41) This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110> IIDA, Shigeru
SATOH, Mitsuo
INOUE, Miho
WAKITANI, Masako
UCHIDA, Kazuhisa
NIWA, Rinpei
SHITARA, Kenya

<120> Ganglioside GM2-specific antibody composition

<130> Q105982

<140> 10575114
<141> 2008-06-09

<150> P2003-350168
<151> 2003-10-09

<150> P2004-129431
<151> 2004-04-26

<150> PCT/JP04/15317
<151> 2004-10-08

<160> 43

<170> PatentIn Ver. 2.1

<210> 1
<211> 1504
<212> DNA
<213> Cricetulus griseus

<220>
<221> CDS
<222> (1)..(1119)

<400> 1
```
atg gct cac gct ccc gct agc tgc ccg agc tcc agg aac tct ggg gac   48
Met Ala His Ala Pro Ala Ser Cys Pro Ser Ser Arg Asn Ser Gly Asp
  1               5                  10                  15

ggc gat aag ggc aag ccc agg aag gtg gcg ctc atc acg ggc atc acc   96
Gly Asp Lys Gly Lys Pro Arg Lys Val Ala Leu Ile Thr Gly Ile Thr
             20                  25                  30

ggc cag gat ggc tca tac ttg gca gaa ttc ctg ctg gag aaa gga tac   144
Gly Gln Asp Gly Ser Tyr Leu Ala Glu Phe Leu Leu Glu Lys Gly Tyr
         35                  40                  45

gag gtt cat gga att gta cgg cga tcc agt tca ttt aat aca ggt cga   192
Glu Val His Gly Ile Val Arg Arg Ser Ser Ser Phe Asn Thr Gly Arg
     50                  55                  60
```

```
att gaa cat tta tat aag aat cca cag gct cat att gaa gga aac atg   240
Ile Glu His Leu Tyr Lys Asn Pro Gln Ala His Ile Glu Gly Asn Met
 65                  70                  75                  80

aag ttg cac tat ggt gac ctc acc gac agc acc tgc cta gta aaa atc   288
Lys Leu His Tyr Gly Asp Leu Thr Asp Ser Thr Cys Leu Val Lys Ile
                 85                  90                  95

atc aat gaa gtc aaa cct aca gag atc tac aat ctt ggt gcc cag agc   336
Ile Asn Glu Val Lys Pro Thr Glu Ile Tyr Asn Leu Gly Ala Gln Ser
            100                 105                 110

cat gtc aag att tcc ttt gac tta gca gag tac act gca gat gtt gat   384
His Val Lys Ile Ser Phe Asp Leu Ala Glu Tyr Thr Ala Asp Val Asp
        115                 120                 125

gga gtt ggc acc ttg cgg ctt ctg gat gca att aag act tgt ggc ctt   432
Gly Val Gly Thr Leu Arg Leu Leu Asp Ala Ile Lys Thr Cys Gly Leu
    130                 135                 140

ata aat tct gtg aag ttc tac cag gcc tca act agt gaa ctg tat gga   480
Ile Asn Ser Val Lys Phe Tyr Gln Ala Ser Thr Ser Glu Leu Tyr Gly
145                 150                 155                 160

aaa gtg caa gaa ata ccc cag aaa gag acc acc cct ttc tat cca agg   528
Lys Val Gln Glu Ile Pro Gln Lys Glu Thr Thr Pro Phe Tyr Pro Arg
                165                 170                 175

tcg ccc tat gga gca gcc aaa ctt tat gcc tat tgg att gta gtg aac   576
Ser Pro Tyr Gly Ala Ala Lys Leu Tyr Ala Tyr Trp Ile Val Val Asn
            180                 185                 190

ttt cga gag gct tat aat ctc ttt gcg gtg aac ggc att ctc ttc aat   624
Phe Arg Glu Ala Tyr Asn Leu Phe Ala Val Asn Gly Ile Leu Phe Asn
        195                 200                 205

cat gag agt cct aga aga gga gct aat ttt gtt act cga aaa att agc   672
His Glu Ser Pro Arg Arg Gly Ala Asn Phe Val Thr Arg Lys Ile Ser
    210                 215                 220

cgg tca gta gct aag att tac ctt gga caa ctg gaa tgt ttc agt ttg   720
Arg Ser Val Ala Lys Ile Tyr Leu Gly Gln Leu Glu Cys Phe Ser Leu
225                 230                 235                 240

gga aat ctg gac gcc aaa cga gac tgg ggc cat gcc aag gac tat gtc   768
Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val
                245                 250                 255

gag gct atg tgg ctg atg tta caa aat gat gaa cca gag gac ttt gtc   816
Glu Ala Met Trp Leu Met Leu Gln Asn Asp Glu Pro Glu Asp Phe Val
            260                 265                 270

ata gct act ggg gaa gtt cat agt gtc cgt gaa ttt gtt gag aaa tca   864
Ile Ala Thr Gly Glu Val His Ser Val Arg Glu Phe Val Glu Lys Ser
        275                 280                 285
```

```
ttc atg cac att gga aag acc att gtg tgg gaa gga aag aat gaa aat   912
Phe Met His Ile Gly Lys Thr Ile Val Trp Glu Gly Lys Asn Glu Asn
    290                 295                 300

gaa gtg ggc aga tgt aaa gag acc ggc aaa att cat gtg act gtg gat   960
Glu Val Gly Arg Cys Lys Glu Thr Gly Lys Ile His Val Thr Val Asp
305                 310                 315                 320

ctg aaa tac tac cga cca act gaa gtg gac ttc ctg cag gga gac tgc   1008
Leu Lys Tyr Tyr Arg Pro Thr Glu Val Asp Phe Leu Gln Gly Asp Cys
                325                 330                 335

tcc aag gcg cag cag aaa ctg aac tgg aag ccc cgc gtt gcc ttt gac   1056
Ser Lys Ala Gln Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp
            340                 345                 350

gag ctg gtg agg gag atg gtg caa gcc gat gtg gag ctc atg aga acc   1104
Glu Leu Val Arg Glu Met Val Gln Ala Asp Val Glu Leu Met Arg Thr
        355                 360                 365

aac ccc aac gcc tga gcacctctac aaaaaaattc gcgagacatg gactatggtg   1159
Asn Pro Asn Ala
    370

cagagccagc caaccagagt ccagccactc ctgagaccat cgaccataaa ccctcgactg 1219
cctgtgtcgt ccccacagct aagagctggg ccacaggttt gtgggcacca ggacggggac 1279
actccagagc taaggccact tcgcttttgt caaaggctcc tctcaatgat tttgggaaat 1339
caagaagttt aaaatcacat actcatttta cttgaaatta tgtcactaga caacttaaat 1399
ttttgagtct tgagattgtt tttctctttt cttattaaat gatctttcta tgacccagca 1459
aaaaaaaaaa aaaaaaggga tataaaaaaa aaaaaaaaaa aaaaa                 1504


<210> 2
<211> 372
<212> PRT
<213> Cricetulus griseus

<400> 2
Met Ala His Ala Pro Ala Ser Cys Pro Ser Ser Arg Asn Ser Gly Asp
  1               5                  10                  15

Gly Asp Lys Gly Lys Pro Arg Lys Val Ala Leu Ile Thr Gly Ile Thr
             20                  25                  30

Gly Gln Asp Gly Ser Tyr Leu Ala Glu Phe Leu Leu Glu Lys Gly Tyr
         35                  40                  45

Glu Val His Gly Ile Val Arg Arg Ser Ser Ser Phe Asn Thr Gly Arg
     50                  55                  60

Ile Glu His Leu Tyr Lys Asn Pro Gln Ala His Ile Glu Gly Asn Met
 65                  70                  75                  80

Lys Leu His Tyr Gly Asp Leu Thr Asp Ser Thr Cys Leu Val Lys Ile
                 85                  90                  95

Ile Asn Glu Val Lys Pro Thr Glu Ile Tyr Asn Leu Gly Ala Gln Ser
```

```
            100                 105                 110

His Val Lys Ile Ser Phe Asp Leu Ala Glu Tyr Thr Ala Asp Val Asp
        115                 120                 125

Gly Val Gly Thr Leu Arg Leu Leu Asp Ala Ile Lys Thr Cys Gly Leu
    130                 135                 140

Ile Asn Ser Val Lys Phe Tyr Gln Ala Ser Thr Ser Glu Leu Tyr Gly
145                 150                 155                 160

Lys Val Gln Glu Ile Pro Gln Lys Glu Thr Thr Pro Phe Tyr Pro Arg
                165                 170                 175

Ser Pro Tyr Gly Ala Ala Lys Leu Tyr Ala Tyr Trp Ile Val Val Asn
            180                 185                 190

Phe Arg Glu Ala Tyr Asn Leu Phe Ala Val Asn Gly Ile Leu Phe Asn
        195                 200                 205

His Glu Ser Pro Arg Arg Gly Ala Asn Phe Val Thr Arg Lys Ile Ser
    210                 215                 220

Arg Ser Val Ala Lys Ile Tyr Leu Gly Gln Leu Glu Cys Phe Ser Leu
225                 230                 235                 240

Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val
                245                 250                 255

Glu Ala Met Trp Leu Met Leu Gln Asn Asp Glu Pro Glu Asp Phe Val
            260                 265                 270

Ile Ala Thr Gly Glu Val His Ser Val Arg Glu Phe Val Glu Lys Ser
        275                 280                 285

Phe Met His Ile Gly Lys Thr Ile Val Trp Glu Gly Lys Asn Glu Asn
    290                 295                 300

Glu Val Gly Arg Cys Lys Glu Thr Gly Lys Ile His Val Thr Val Asp
305                 310                 315                 320

Leu Lys Tyr Tyr Arg Pro Thr Glu Val Asp Phe Leu Gln Gly Asp Cys
                325                 330                 335

Ser Lys Ala Gln Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp
            340                 345                 350

Glu Leu Val Arg Glu Met Val Gln Ala Asp Val Glu Leu Met Arg Thr
        355                 360                 365

Asn Pro Asn Ala
    370


<210> 3
<211> 1316
<212> DNA
```

<213> Cricetulus griseus

<400> 3
gccccgcccc ctccacctgg accgagagta gctggagaat tgtgcaccgg aagtagctct 60

tggactggtg gaaccctgcg caggtgcagc aacaatgggt gagccccagg gatccaggag 120

gatcctagtg acaggggggct ctggactggt gggcagagct atccagaagg tggtcgcaga 180

tggcgctggc ttacccggag aggaatgggt gtttgtctcc tccaaagatg cagatctgac 240

ggatgcagca caaacccaag ccctgttcca gaaggtacag cccacccatg tcatccatct 300

tgctgcaatg gtaggaggcc ttttccggaa tatcaaatac aacttggatt tctggaggaa 360

gaatgtgcac atcaatgaca acgtcctgca ctcagctttc gaggtgggca ctcgcaaggt 420

ggtctcctgc ctgtccacct gtatcttccc tgacaagacc acctatccta ttgatgaaac 480

aatgatccac aatggtccac cccacagcag caattttggg tactcgtatg ccaagaggat 540

gattgacgtg cagaacaggg cctacttcca gcagcatggc tgcaccttca ctgctgtcat 600

ccctaccaat gtctttggac ctcatgacaa cttcaacatt gaagatggcc atgtgctgcc 660

tggcctcatc cataaggtgc atctggccaa gagtaatggt tcagccttga ctgtttgggg 720

tacagggaaa ccacggaggc agttcatcta ctcactggac ctagcccggc tcttcatctg 780

ggtcctgcgg gagtacaatg aagttgagcc catcatcctc tcagtgggcg aggaagatga 840

agtctccatt aaggaggcag ctgaggctgt agtggaggcc atggacttct gtggggaagt 900

cacttttgat tcaacaaagt cagatgggca gtataagaag acagccagca atggcaagct 960

tcgggcctac ttgcctgatt tccgtttcac acccttcaag caggctgtga aggagacctg 1020

tgcctggttc accgacaact atgagcaggc ccggaagtga agcatgggac aagcgggtgc 1080

tcagctggca atgcccagtc agtaggctgc agtctcatca tttgcttgtc aagaactgag 1140

gacagtatcc agcaacctga gccacatgct ggtctctctg ccaggggggct tcatgcagcc 1200

atccagtagg gcccatgttt gtccatcctc gggggaaggc cagaccaaca ccttgtttgt 1260

ctgcttctgc cccaacctca gtgcatccat gctggtcctg ctgtcccttg tctaga 1316

<210> 4
<211> 321
<212> PRT
<213> Cricetulus griseus

<400> 4
Met Gly Glu Pro Gln Gly Ser Arg Arg Ile Leu Val Thr Gly Gly Ser
 1   5   10   15

```
Gly Leu Val Gly Arg Ala Ile Gln Lys Val Val Ala Asp Gly Ala Gly
             20                  25                  30

Leu Pro Gly Glu Glu Trp Val Phe Val Ser Ser Lys Asp Ala Asp Leu
         35                  40                  45

Thr Asp Ala Ala Gln Thr Gln Ala Leu Phe Gln Lys Val Gln Pro Thr
     50                  55                  60

His Val Ile His Leu Ala Ala Met Val Gly Gly Leu Phe Arg Asn Ile
 65                  70                  75                  80

Lys Tyr Asn Leu Asp Phe Trp Arg Lys Asn Val His Ile Asn Asp Asn
                 85                  90                  95

Val Leu His Ser Ala Phe Glu Val Gly Thr Arg Lys Val Val Ser Cys
            100                 105                 110


Leu Ser Thr Cys Ile Phe Pro Asp Lys Thr Thr Tyr Pro Ile Asp Glu
        115                 120                 125

Thr Met Ile His Asn Gly Pro Pro His Ser Ser Asn Phe Gly Tyr Ser
    130                 135                 140

Tyr Ala Lys Arg Met Ile Asp Val Gln Asn Arg Ala Tyr Phe Gln Gln
145                 150                 155                 160

His Gly Cys Thr Phe Thr Ala Val Ile Pro Thr Asn Val Phe Gly Pro
                165                 170                 175

His Asp Asn Phe Asn Ile Glu Asp Gly His Val Leu Pro Gly Leu Ile
            180                 185                 190

His Lys Val His Leu Ala Lys Ser Asn Gly Ser Ala Leu Thr Val Trp
        195                 200                 205

Gly Thr Gly Lys Pro Arg Arg Gln Phe Ile Tyr Ser Leu Asp Leu Ala
    210                 215                 220

Arg Leu Phe Ile Trp Val Leu Arg Glu Tyr Asn Glu Val Glu Pro Ile
225                 230                 235                 240

Ile Leu Ser Val Gly Glu Glu Asp Glu Val Ser Ile Lys Glu Ala Ala
                245                 250                 255

Glu Ala Val Val Glu Ala Met Asp Phe Cys Gly Glu Val Thr Phe Asp
            260                 265                 270

Ser Thr Lys Ser Asp Gly Gln Tyr Lys Lys Thr Ala Ser Asn Gly Lys
        275                 280                 285

Leu Arg Ala Tyr Leu Pro Asp Phe Arg Phe Thr Pro Phe Lys Gln Ala
    290                 295                 300


Val Lys Glu Thr Cys Ala Trp Phe Thr Asp Asn Tyr Glu Gln Ala Arg
```

305 310 315 320

Lys

<210> 5
<211> 2008
<212> DNA
<213> Cricetulus griseus

<400> 5
aacagaaact tattttcctg tgtggctaac tagaaccaga gtacaatgtt tccaattctt 60

tgagctccga gaagacagaa gggagttgaa actctgaaaa tgcgggcatg gactggttcc 120

tggcgttgga ttatgctcat tctttttgcc tgggggacct tattgtttta tataggtggt 180

catttggttc gagataatga ccaccctgac cattctagca gagaactctc caagattctt 240

gcaaagctgg agcgcttaaa acaacaaaat gaagacttga ggagaatggc tgagtctctc 300

cgaataccag aaggccctat tgatcagggg acagctacag gaagagtccg tgttttagaa 360

gaacagcttg ttaaggccaa agaacagatt gaaaattaca agaaacaagc taggaatgat 420

ctgggaaagg atcatgaaat cttaaggagg aggattgaaa atggagctaa agagctctgg 480

ttttttctac aaagtgaatt gaagaaatta aagaaattag aaggaaacga actccaaaga 540

catgcagatg aaattctttt ggatttagga catcatgaaa ggtctatcat gacagatcta 600

tactacctca gtcaaacaga tggagcaggt gagtggcggg aaaaagaagc caaagatctg 660

acagagctgg tccagcggag aataacatat ctgcagaatc ccaaggactg cagcaaagcc 720

agaaagctgg tatgtaatat caacaaaggc tgtggctatg gatgtcaact ccatcatgtg 780

gtttactgct tcatgattgc ttatggcacc cagcgaacac tcatcttgga atctcagaat 840

tggcgctatg ctactggagg atgggagact gtgtttagac ctgtaagtga gacatgcaca 900

gacaggtctg gcctctccac tggacactgg tcaggtgaag tgaaggacaa aaatgttcaa 960

gtggtcgagc tccccattgt agacagcctc catcctcgtc ctccttactt acccttggct 1020

gtaccagaag accttgcaga tcgactcctg agagtccatg gtgatcctgc agtgtggtgg 1080

gtatcccagt ttgtcaaata cttgatccgt ccacaacctt ggctggaaag ggaaatagaa 1140

gaaaccacca agaagcttgg cttcaaacat ccagttattg gagtccatgt cagacgcact 1200

gacaaagtgg gaacagaagc agccttccat cccattgagg aatacatggt acacgttgaa 1260

gaacattttc agcttctcga acgcagaatg aaagtggata aaaaaagagt gtatctggcc 1320

actgatgacc cttctttgtt aaaggaggca aagacaaagt actccaatta tgaatttatt 1380

agtgataact ctatttcttg gtcagctgga ctacacaacc gatacacaga aaattcactt 1440

cggggcgtga tcctggatat acactttctc tcccaggctg acttccttgt gtgtactttt 1500

tcatcccagg tctgtagggt tgcttatgaa atcatgcaaa cactgcatcc tgatgcctct 1560

gcaaacttcc attctttaga tgacatctac tattttggag gccaaaatgc ccacaaccag 1620

attgcagttt atcctcacca acctcgaact aaagaggaaa tccccatgga acctggagat 1680

atcattggtg tggctggaaa ccattggaat ggttactcta aaggtgtcaa cagaaaacta 1740

ggaaaaacag gcctgtaccc ttcctacaaa gtccgagaga agatagaaac agtcaaatac 1800

cctacatatc ctgaagctga aaaatagaga tggagtgtaa gagattaaca acagaattta 1860

gttcagacca tctcagccaa gcagaagacc cagactaaca tatggttcat tgacagacat 1920

gctccgcacc aagagcaagt gggaaccctc agatgctgca ctggtggaac gcctctttgt 1980

gaagggctgc tgtgccctca agcccatg 2008

<210> 6
<211> 1728
<212> DNA
<213> Mus musculus

<400> 6
atgcgggcat ggactggttc ctggcgttgg attatgctca ttctttttgc ctgggggacc 60

ttgttatttt atataggtgg tcatttggtt cgagataatg accaccctga tcactccagc 120

agagaactct ccaagattct tgcaaagctt gaacgcttaa aacagcaaaa tgaagacttg 180

aggcgaatgg ctgagtctct ccgaatacca gaaggcccca ttgaccaggg gacagctaca 240

ggaagagtcc gtgttttaga agaacagctt gttaaggcca aagaacagat tgaaaattac 300

aagaaacaag ctagaaatgg tctggggaag gatcatgaaa tcttaagaag gaggattgaa 360

aatggagcta aagagctctg gttttttcta caaagcgaac tgaagaaatt aaagcattta 420

gaaggaaatg aactccaaag acatgcagat gaaattcttt tggatttagg acaccatgaa 480

aggtctatca tgacagatct atactacctc agtcaaacag atggagcagg ggattggcgt 540

gaaaaagagg ccaaagatct gacagagctg gtccagcgga gaataacata tctccagaat 600

cctaaggact gcagcaaagc caggaagctg gtgtgtaaca tcaataaagg ctgtggctat 660

ggttgtcaac tccatcacgt ggtctactgt ttcatgattg cttatggcac ccagcgaaca 720

ctcatcttgg aatctcagaa ttggcgctat gctactggtg gatgggagac tgtgtttaga 780

cctgtaagtg agacatgtac agacagatct ggcctctcca ctggacactg gtcaggtgaa 840

gtaaatgaca aaaacattca agtggtcgag ctccccattg tagacagcct ccatcctcgg 900

cctccttact taccactggc tgttccagaa gaccttgcag accgactcct aagagtccat 960

ggtgaccctg cagtgtggtg ggtgtcccag tttgtcaaat acttgattcg tccacaacct 1020

tggctggaaa aggaaataga agaagccacc aagaagcttg gcttcaaaca tccagttatt 1080

ggagtccatg tcagacgcac agacaaagtg ggaacagaag cagccttcca ccccatcgag 1140

gagtacatgg tacacgttga agaacatttt cagcttctcg cacgcagaat gcaagtggat 1200

aaaaaaagag tatatctggc tactgatgat cctactttgt taaaggaggc aaagacaaag 1260

tactccaatt atgaatttat tagtgataac tctatttctt ggtcagctgg actacacaat 1320

cggtacacag aaaattcact tcggggtgtg atcctggata tacactttct ctcacaggct 1380

gactttctag tgtgtacttt ttcatcccag gtctgtcggg ttgcttatga aatcatgcaa 1440

accctgcatc ctgatgcctc tgcgaacttc cattctttgg atgacatcta ctattttgga 1500

ggccaaaatg cccacaatca gattgctgtt tatcctcaca aacctcgaac tgaagaggaa 1560

attccaatgg aacctggaga tatcattggt gtggctggaa accattggga tggttattct 1620

aaaggtatca acagaaaact tggaaaaaca ggcttatatc cctcctacaa agtccgagag 1680

aagatagaaa cagtcaagta tcccacatat cctgaagctg aaaaatag 1728

<210> 7
<211> 575
<212> PRT
<213> Cricetulus griseus

<400> 7
Met Arg Ala Trp Thr Gly Ser Trp Arg Trp Ile